



SEQUENCE LISTING

<110> FRENCH, Cynthia K.
YAMAMOTO, Karen K.
EL SHAMI, A. Said

<120> Prostate Cancer-Specific Marker

<130> 107-206-C-D

<140> to be assigned

<141> 2003-08-26

<150> 60/041,246

<151> 1997-03-07

<150> 60/047,811

<151> 1997-05-15

<150> 09/036,315

<151> 1998-03-06

<150> 09/535,597

<151> 2000-03-27

<150> 09/680,121

<151> 2000-10-04

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<170> PatentIn Ver. 2.1

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<222> (151)..(1425)

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cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
Met Ala Pro Ile Thr Thr Ser Arg
1 5

gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
10 15 20

ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 270
Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
25 30 35 40

aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
45 50 55

ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
60 65 70

ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 414
Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
75 80 85

aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat 462
Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
90 95 100

ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat 510
Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
105 110 115 120

gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct 558
Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
125 130 135

gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag 606
Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
140 145 150

aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa 654
Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
155 160 165

01 Sequence Listing for 107-206-C-D.txt

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 Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro
 185 190 195 200

gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat 798
 Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp
 205 210 215

cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa 846
 Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln
 220 225 230

atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt 894
 Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe
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tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att 942
 Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile
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aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc 1038
 Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
 285 290 295

tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga 1086
 Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
 300 305 310

cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa 1134
 His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
 315 320 325

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 Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
 330 335 340

gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt 1230
 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
 345 350 355 360

gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt 1278
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 365 370 375

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 380 385 390

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 395 400 405

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 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
 410 415 420

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 Gly
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          20             25             30

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Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
          35             40             45

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Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
  50             55             60

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Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
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Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
          85             90             95

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Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
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Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
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Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
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Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
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 165 170 175
 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
 180 185 190
 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
 195 200 205
 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
 210 215 220
 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
 225 230 235 240
 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
 245 250 255
 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
 260 265 270
 Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
 275 280 285
 Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
 290 295 300
 Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
 305 310 315 320
 Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
 325 330 335
 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
 340 345 350
 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
 355 360 365
 Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
 370 375 380
 Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
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Ala Lys Trp His Val Leu Cys Asp Gly
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 35 40 45
 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
 50 55 60
 Glu Asn Leu Ser Ser Lys Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu
 65 70 75 80
 Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu
 85 90 95
 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Pro Lys Ala
 100 105 110
 Gly Ser Ser Ser Asp Leu Glu Asn Val Thr Pro Lys Leu Phe Pro Glu
 115 120 125
 Thr Glu Lys Glu Ala Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
 130 135 140
 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Leu Ser
 145 150 155 160
 Leu Glu Tyr Asn Phe Glu Lys Lys Ala Phe Val Val Asn Ile Lys Glu
 165 170 175
 Ala Gln Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
 180 185 190
 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
 195 200 205
 Arg Val Leu Arg Lys Thr Leu Asp Pro Val Phe Asp Glu Thr Phe Thr
 210 215 220
 Phe Tyr Gly Val Pro Tyr Pro His Ile Gln Glu Leu Ser Leu His Phe
 225 230 235 240
 Thr Val Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Val Ile Gly Glu
 245 250 255
 Val Leu Val Pro Leu Ser Gly Ile Glu Leu Ser Asp Gly Lys Met Leu
 260 265 270

Met Thr Arg Glu Ile Ile Lys Arg Asn Ala Lys Lys Ser Ser Gly Arg
275 280 285

Gly Glu Leu Leu Val Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
325 330 335

Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
340 345 350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu
355 360 365

Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
370 375 380

Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser
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Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile
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Ala Lys Trp His Met Leu Cys Asp Gly
420 425

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<213> Homo sapiens

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<221> PEPTIDE

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<223> PKC-C2 internal repeat (amino acid positions
154-271)

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1 5 10 15

Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln

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Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser					
	35		40		45
Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser					
	50		55		60
Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn					
	65		70		75
					80
Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile					
		85		90	95
Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met					
	100		105		110
Gly Ala Leu Ser Phe					
	115				

<210> 7
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 <212> PRT
 <213> Homo sapiens
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 <223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino
 acid) positions 276-397

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 Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu
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 Leu Ile Ser Leu Cys Tyr Gln Ser Thr Ile Asn Thr Leu Thr Val Val
 20 25 30
 Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
 35 40 45
 Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
 50 55 60
 Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
 65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
 85 90 95

Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val
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Ile Gly Gln Leu Val Leu Gly Ala Ala
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<210> 8

<211> 115

<212> PRT

<213> rat

<220>

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<222> (1)..(115)

<223> synaptotagmin "B" internal repeat (amino acid
 positions 268-383)

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Val Pro Thr Ala Gly Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn
 20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
 35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
 50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
 65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
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Gly Tyr Asn
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 <223> synaptotagmin "A" internal repeat (amino acid
 positions 134-254)

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 20 25 30

Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr
 35 40 45

Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Phe Glu Thr Lys
 50 55 60

Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe
 65 70 75 80

Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val
 85 90 95

Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys
 100 105 110

Val Pro Met Asn Thr Val Asp Phe
 115 120

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acid positions 150-263)

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Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr
 35 40 45

Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys
 50 55 60

Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro
 65 70 75 80

Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe
 85 90 95

Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu
 100 105 110

Ser

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<213> Homo sapiens

<220>

<223> residue 1=Thr, Ser or Met

<220>

<223> residue 2=Asp, Glu, Ala, Ser or Thr

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<210> 12

<211> 10

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<213> Homo sapiens

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<223> residue 1=Thr, Ser or Met

<220>

<223> residue 2=Asp, Glu, Ala, Ser or Thr

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1 5 10

<210> 13

<211> 7

<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<223> residue 1=Glu or Asp

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1 5

<210> 15

<211> 9

<212> PRT

<213> Homo sapiens

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<223> residue 2=Leu, Met, Ile, Val, Ser, Ala, Thr, Phe,
Cys, Gly, Asp or Glu

<220>

<223> residue 9=Lys, Arg or Tyr

<400> 15

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<213> Homo sapiens

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Cys, Gly, Asp or Glu

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<223> residue 10=Lys, Arg or Tyr

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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5

10

<210> 17

<211> 9

<212> PRT

<213> Homo sapiens

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<223> residue 2=Thr or Val

<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys

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<210> 18

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Thr or Val

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<210> 19
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 <212> PRT
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 <223> residue 2=Tyr, Phe or Trp

<220>
 <223> residue 9=Phe, Ile, Trp, Met or Leu

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 <212> PRT
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 1 5 10

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Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln
 20 25 30

<210> 22
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Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys Phe
 20 25 30

Gly Ala

<210> 23
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<400> 23
 Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu Gly
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Glu Lys Glu Ser Val Ser Pro Glu Ser
 20 25

<210> 24
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 <212> PRT
 <213> Homo sapiens

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 1 5 10 15

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 20 25 30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp
 35 40 45

Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu
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 Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu
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 Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu
 20 25 30

<210> 27
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 <212> PRT
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<220>
 <223> residue 5=Val or Ile

<400> 27
 Ser Asp Pro Tyr Xaa Lys
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